



IFWO

RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/784,089

TIME: 14:54:11

Input Set : N:\Crf3\RULE60\10784089.raw.txt

Output Set: N:\CRF4\08302004\J784089.raw

1 <110> APPLICANT: Millennium Pharmaceuticals, Inc.
 2 Meyers, Rachel
 3 Silos-Santiago, Inmaculada
 4 <120> TITLE OF INVENTION: 32544, a novel human phospholipase C and
 5 uses thereof
 6 <130> FILE REFERENCE: 38155-20048.00
 7 <140> CURRENT APPLICATION NUMBER: US/10/784,089
 8 <141> CURRENT FILING DATE: 2004-02-20
 9 <150> PRIOR APPLICATION NUMBER: US/09/927,112
 10 <151> PRIOR FILING DATE: 2001-08-10
 11 <150> PRIOR APPLICATION NUMBER: US 60/246,808
 12 <151> PRIOR FILING DATE: 2000-11-08
 13 <160> NUMBER OF SEQ ID NOS: 17
 14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 4635
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (435)...(4058)
 23 <400> SEQUENCE: 1

24	tcgcgatcta gaactagtgg cacggctcct gcactccac	tgccgcagga actgctcagg	60
25	aacctgccgg tctccggctg ggacgggtggc tggatcagct	caagcctcca gggccctgag	120
26	gctgaggggc tgagtgtca ttccagccgc ctccggggaac	ccgggctggg agaccccatg	180
27	cctgggggtg agcctggagc cagggcagtg cggtagagg	ctccggagag agggctgggc	240
28	accaccaggc ttgggtgtgt gatgcgtgc tggcccaggc	tacacccga caagggacac	300
29	cgggggccct gggagcagat agacctcaga gcagcctcct	cctgcctcct gtggacggcc	360
30	ggccccagct ggtgatccca gccagtccca gctttcagtt	gctgccccca cggacagtcc	420
31	tcagtccctc catg atg gct ccc ccg aca gcc ggc	ccc ctt cct ggc cca	470
32		Met Ala Pro Pro Thr Ala Gly Pro Leu Pro Gly Pro	
33		1 5 10	
34	gct ctt ccg cct gag gac cca ggg ccg gat ccg	gag agc agg tgg ctt	518
35	Ala Leu Pro Pro Glu Asp Pro Gly Pro Asp Pro	Glu Ser Arg Trp Leu	
36		15 20 25	
37	ttc ttg agc gcc aac att ctg ccc gtg gtg gag	cgg tgc atg ggt gcc	566
38	Phe Leu Ser Ala Asn Ile Leu Pro Val Val Glu	Arg Cys Met Gly Ala	
39		30 35 40	
40	atg caa gag ggg atg cag atg gtg aag ctg cgt	ggc ggc tcc aag ggc	614
41	Met Gln Glu Gly Met Gln Met Val Lys Leu Arg	Gly Gly Ser Lys Gly	
42		45 50 55 60	
43	ctg gtc cgc ttc tac ctg gac gag cac cgc	tcc tgc atc cgc tgg	662
44	Leu Val Arg Phe Tyr Tyr Leu Asp Glu His Arg	Ser Cys Ile Arg Trp	

ENTERED

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45					65					70					75		
46	agg	ccc	tca	cgc	aag	aac	gag	aag	gcc	aag	atc	tcc	atc	gac	tcc	atc	710
47	Arg	Pro	Ser	Arg	Lys	Asn	Glu	Lys	Ala	Lys	Ile	Ser	Ile	Asp	Ser	Ile	
48					80					85					90		
49	cag	gag	gtg	agt	gag	ggg	cgg	cag	tcg	gag	gtc	ttc	cag	cgc	tac	cct	758
50	Gln	Glu	Val	Ser	Glu	Gly	Arg	Gln	Ser	Glu	Val	Phe	Gln	Arg	Tyr	Pro	
51					95					100					105		
52	gac	ggc	agc	ttc	gac	ccc	aac	tgc	tgc	ttc	agc	atc	tac	cac	ggc	agc	806
53	Asp	Gly	Ser	Phe	Asp	Pro	Asn	Cys	Cys	Phe	Ser	Ile	Tyr	His	Gly	Ser	
54					110					115					120		
55	cac	cgc	gag	tcg	ctg	gac	ctg	gtc	tcc	acc	agc	agc	gag	gtg	gcg	cgc	854
56	His	Arg	Glu	Ser	Leu	Asp	Leu	Val	Ser	Thr	Ser	Ser	Glu	Val	Ala	Arg	
57										125					130		
58	acc	tgg	gtc	act	ggc	ctg	cgc	tac	ctc	atg	gcc	ggc	atc	agc	gac	gag	902
59	Thr	Trp	Val	Thr	Gly	Leu	Arg	Tyr	Leu	Met	Ala	Gly	Ile	Ser	Asp	Glu	
60										145					150		
61	gac	agc	ctg	gct	cgc	cgc	cag	cgc	acc	agg	gac	cag	tgg	ctg	aag	cag	950
62	Asp	Ser	Leu	Ala	Arg	Arg	Gln	Arg	Thr	Arg	Asp	Gln	Trp	Leu	Lys	Gln	
63					160					165					170		
64	acg	ttt	gac	gag	gcc	gac	aag	aac	ggg	gat	ggc	agc	ctg	agc	att	ggc	998
65	Thr	Phe	Asp	Glu	Ala	Asp	Lys	Asn	Gly	Asp	Gly	Ser	Leu	Ser	Ile	Gly	
66					175					180					185		
67	gag	gtc	ctg	cag	ctg	ctg	cac	aag	ctc	aac	gtg	aac	ctg	ccc	cgg	cag	1046
68	Glu	Val	Leu	Gln	Leu	Leu	His	Lys	Leu	Asn	Val	Asn	Leu	Pro	Arg	Gln	
69										190					195		
70	agg	gtg	aag	cag	atg	ttc	agg	gaa	gcg	gac	acg	gat	gac	cac	caa	ggg	1094
71	Arg	Val	Lys	Gln	Met	Phe	Arg	Glu	Ala	Asp	Thr	Asp	Asp	His	Gln	Gly	
72										205					210		
73	acg	ctg	ggt	ttt	gaa	gag	ttc	tgt	gcc	ttc	tac	aag	atg	atg	tcc	acc	1142
74	Thr	Leu	Gly	Phe	Glu	Glu	Phe	Cys	Ala	Phe	Tyr	Lys	Met	Met	Ser	Thr	
75										225					230		
76	cgc	cgg	gac	ctc	tac	ctg	ctc	atg	ctg	acc	tac	agc	aac	cac	aag	gac	1190
77	Arg	Arg	Asp	Leu	Tyr	Leu	Leu	Met	Leu	Thr	Tyr	Ser	Asn	His	Lys	Asp	
78					240					245					250		
79	cac	ctg	gat	gcc	gcc	agc	ctg	cag	cgc	ttc	ctg	cag	gtg	gag	cag	aag	1238
80	His	Leu	Asp	Ala	Ala	Ser	Leu	Gln	Arg	Phe	Leu	Gln	Val	Glu	Gln	Lys	
81					255					260					265		
82	atg	gcg	ggt	gtg	acc	ctc	gag	agc	tgc	cag	gac	atc	atc	gag	cag	ttt	1286
83	Met	Ala	Gly	Val	Thr	Leu	Glu	Ser	Cys	Gln	Asp	Ile	Ile	Glu	Gln	Phe	
84										270					275		
85	gag	cca	tgc	cca	gaa	aac	aag	agt	aag	ggg	ctg	ctg	ggc	att	gat	ggc	1334
86	Glu	Pro	Cys	Pro	Glu	Asn	Lys	Ser	Lys	Gly	Leu	Leu	Gly	Ile	Asp	Gly	
87										285					290		
88	ttc	acc	aac	tac	acc	agg	agc	cct	gct	ggt	gac	atc	ttc	aac	cct	gag	1382
89	Phe	Thr	Asn	Tyr	Thr	Arg	Ser	Pro	Ala	Gly	Asp	Ile	Phe	Asn	Pro	Glu	
90										305					310		
91	cac	cac	cat	gtg	cac	cag	gac	atg	acg	cag	ccg	ctg	agc	cac	tac	ttc	1430
92	His	His	His	Val	His	Gln	Asp	Met	Thr	Gln	Pro	Leu	Ser	His	Tyr	Phe	
93					320					325					330		

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94	atc acc tgc tcc cac aac acc tac ctc gtg ggt gac cag ctc atg tcc	1478
95	Ile Thr Ser Ser His Asn Thr Tyr Leu Val Gly Asp Gln Leu Met Ser	
96	335 340 345	
97	cag tca cgg gtg gac atg tat gct tgg gtc ctg cag gct ggc tgc cgc	1526
98	Gln Ser Arg Val Asp Met Tyr Ala Trp Val Leu Gln Ala Gly Cys Arg	
99	350 355 360	
100	tgc gtg gag gtg gac tgc tgg gat ggg ccc gac ggg gag ccc att gtg	1574
101	Cys Val Glu Val Asp Cys Trp Asp Gly Pro Asp Gly Glu Pro Ile Val	
102	365 370 375 380	
103	cac cat ggc tac act ctg act tcc aag atc ctc ttc aaa gac gtc att	1622
104	His His Gly Tyr Thr Leu Thr Ser Lys Ile Leu Phe Lys Asp Val Ile	
105	385 390 395	
106	gaa acc atc aac aaa tat gcc ttc atc aag aat gag tac cca gtg atc	1670
107	Glu Thr Ile Asn Lys Tyr Ala Phe Ile Lys Asn Glu Tyr Pro Val Ile	
108	400 405 410	
109	ctg tcc atc gaa aac cac tgc agt gtc atc cag cag aag aaa atg gcc	1718
110	Leu Ser Ile Glu Asn His Cys Ser Val Ile Gln Gln Lys Lys Met Ala	
111	415 420 425	
112	cag tat ctg act gac atc ctt ggg gac aag ctg gac ctg tca tca gtg	1766
113	Gln Tyr Leu Thr Asp Ile Leu Gly Asp Lys Leu Asp Leu Ser Ser Val	
114	430 435 440	
115	agc agt gaa gat gcc acc aca ctc ccc tct cca cag atg ctc aag ggc	1814
116	Ser Ser Glu Asp Ala Thr Thr Leu Pro Ser Pro Gln Met Leu Lys Gly	
117	445 450 455 460	
118	aag atc ctc gtg aag ggg aag aag ctc cca gcc aac atc agc gag gat	1862
119	Lys Ile Leu Val Lys Gly Lys Lys Leu Pro Ala Asn Ile Ser Glu Asp	
120	465 470 475	
121	gcg gag gaa ggc gag gtg tct gat gag gac agt gct gat gag att gac	1910
122	Ala Glu Glu Gly Glu Val Ser Asp Glu Asp Ser Ala Asp Glu Ile Asp	
123	480 485 490	
124	gat gac tgc aag ctc ctc aat ggg gat gca tcc acc aat cga aag cgt	1958
125	Asp Asp Cys Lys Leu Leu Asn Gly Asp Ala Ser Thr Asn Arg Lys Arg	
126	495 500 505	
127	gta gaa aac act gct aag agg aaa ctg gat tcc ctc atc aaa gag tgc	2006
128	Val Glu Asn Thr Ala Lys Arg Lys Leu Asp Ser Leu Ile Lys Glu Ser	
129	510 515 520	
130	aag att cgg gac tgt gag gac ccc aac aac ttc tcc gtc tcc aca ctg	2054
131	Lys Ile Arg Asp Cys Glu Asp Pro Asn Asn Phe Ser Val Ser Thr Leu	
132	525 530 535 540	
133	tcc cca tct gga aag ctc gga cgc aag agc aag gct gaa gag gac gtg	2102
134	Ser Pro Ser Gly Lys Leu Gly Arg Lys Ser Lys Ala Glu Glu Asp Val	
135	545 550 555	
136	gag tct ggg gag gat gcc ggg gcc agc aga cgc aat ggc cgc ctc gtc	2150
137	Glu Ser Gly Glu Asp Ala Gly Ala Ser Arg Arg Asn Gly Arg Leu Val	
138	560 565 570	
139	gtg gga agc ttc tcc agg cgc aag aag aag ggc agc aag ctg aag aag	2198
140	Val Gly Ser Phe Ser Arg Arg Lys Lys Lys Gly Ser Lys Leu Lys Lys	
141	575 580 585	
142	gcg gcc agc gtg gag gag gga gat gag ggt cag gac tcc ccg gga ggc	2246

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143	Ala Ala Ser Val Glu Glu Gly Asp Glu Gly Gln Asp Ser Pro Gly Gly	
144	590 595 600	
145	cag agc cga ggg gcg acc cgg cag aag aag acc atg aag ctg tcc cgg	2294
146	Gln Ser Arg Gly Ala Thr Arg Gln Lys Lys Thr Met Lys Leu Ser Arg	
147	605 610 615 620	
148	gcc ctg tct gac ctg gtg aag tac acc aag tcc gtg gcc acc cac gac	2342
149	Ala Leu Ser Asp Leu Val Lys Tyr Thr Lys Ser Val Ala Thr His Asp	
150	625 630 635	
151	ata gag atg gag gcg gcg tcc agc tgg cag gtg tcg tcc ttc agc gag	2390
152	Ile Glu Met Glu Ala Ala Ser Ser Trp Gln Val Ser Ser Phe Ser Glu	
153	640 645 650	
154	acc aag gcc cac cag att ctg cag cag aag ccg gcg cag tac cta cgc	2438
155	Thr Lys Ala His Gln Ile Leu Gln Gln Lys Pro Ala Gln Tyr Leu Arg	
156	655 660 665	
157	ttc aac cag cag cag ctg tcc cgc atc tac ccc tcc tcc tac cgt gtg	2486
158	Phe Asn Gln Gln Gln Leu Ser Arg Ile Tyr Pro Ser Ser Tyr Arg Val	
159	670 675 680	
160	gac tcc agc aac tac aac ccg cag ccc ttc tgg aac gcc ggc tgc caa	2534
161	Asp Ser Ser Asn Tyr Asn Pro Gln Pro Phe Trp Asn Ala Gly Cys Gln	
162	685 690 695 700	
163	atg gtt gcc ctg aac tac cag tca gag ggg cgg atg ctg cag ctg aac	2582
164	Met Val Ala Leu Asn Tyr Gln Ser Glu Gly Arg Met Leu Gln Leu Asn	
165	705 710 715	
166	cga gcc aag ttc agc gcc aac ggt ggc tgc ggc tac gta ctg aag cct	2630
167	Arg Ala Lys Phe Ser Ala Asn Gly Gly Cys Gly Tyr Val Leu Lys Pro	
168	720 725 730	
169	ggg tgc atg tgc cag ggc gtg ttc aac ccc aac tcg gag gac ccc ctg	2678
170	Gly Cys Met Cys Gln Gly Val Phe Asn Pro Asn Ser Glu Asp Pro Leu	
171	735 740 745	
172	ccc ggg cag ctg aag aag cag ctg gtg ctg cgg atc atc agt ggc cag	2726
173	Pro Gly Gln Leu Lys Lys Gln Leu Val Leu Arg Ile Ile Ser Gly Gln	
174	750 755 760	
175	cag ctt ccc aag ccg cgc gac tcc atg ctg ggg gac cgt ggg gag atc	2774
176	Gln Leu Pro Lys Pro Arg Asp Ser Met Leu Gly Asp Arg Gly Glu Ile	
177	765 770 775 780	
178	atc gac ccc ttt gtg gag gtg gag atc att ggg ctg cct gtg gac tgc	2822
179	Ile Asp Pro Phe Val Glu Val Glu Ile Ile Gly Leu Pro Val Asp Cys	
180	785 790 795	
181	agc agg gag cag acc cgc gtg gtg gac gac aac ggg ttc aac ccc acc	2870
182	Ser Arg Glu Gln Thr Arg Val Val Asp Asp Asn Gly Phe Asn Pro Thr	
183	800 805 810	
184	tgg gag gag acc ctg gtt ttc atg gtg cac atg ccg gag atc gcg ctg	2918
185	Trp Glu Glu Thr Leu Val Phe Met Val His Met Pro Glu Ile Ala Leu	
186	815 820 825	
187	gtc cgc ttc ctg gtc tgg gac cac gat ccc atc ggg cgt gac ttc att	2966
188	Val Arg Phe Leu Val Trp Asp His Asp Pro Ile Gly Arg Asp Phe Ile	
189	830 835 840	
190	ggc cag agg acg ctg gcc ttc agc agc atg atg cca ggc tac aga cac	3014
191	Gly Gln Arg Thr Leu Ala Phe Ser Ser Met Met Pro Gly Tyr Arg His	

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192	845	850	855	860	
193	gtg tac cta gaa ggg atg gaa gag gcc tcc atc ttc gtg cat gtg gct	3062			
194	Val Tyr Leu Glu Gly Met Glu Glu Ala Ser Ile Phe Val His Val Ala				
195	865 870 875				
196	gtc agt gac atc agc ggt aag gtc aag cag gct ctg ggc cta aaa ggc	3110			
197	Val Ser Asp Ile Ser Gly Lys Val Lys Gln Ala Leu Gly Leu Lys Gly				
198	880 885 890				
199	ctc ttc ctc cga ggc cca aag ccc ggc tcg ctg gac agt cat gct gct	3158			
200	Leu Phe Leu Arg Gly Pro Lys Pro Gly Ser Leu Asp Ser His Ala Ala				
201	895 900 905				
202	ggg cgg ccc ccg gcc cgg ccc tcc gtt agc cag cgg atc ctg cgg cgc	3206			
203	Gly Arg Pro Pro Ala Arg Pro Ser Val Ser Gln Arg Ile Leu Arg Arg				
204	910 915 920				
205	acg gcc agc gcc ccg acc aag agc cag aag ccg ggc cgc agg ggc ttc	3254			
206	Thr Ala Ser Ala Pro Thr Lys Ser Gln Lys Pro Gly Arg Arg Gly Phe				
207	925 930 935 940				
208	ccg gag ctg gtc ctg ggt aca cgg gac aca ggc tcc aag ggg gtg gca	3302			
209	Pro Glu Leu Val Leu Gly Thr Arg Asp Thr Gly Ser Lys Gly Val Ala				
210	945 950 955				
211	gac gat gtg gtg ccc ccc ggg ccc gga cct gct ccg gaa gcc cca gcc	3350			
212	Asp Asp Val Val Pro Pro Gly Pro Gly Pro Ala Pro Glu Ala Pro Ala				
213	960 965 970				
214	cag gag ggg ccc ggc agc ggc agc ccc cga ggt aag gcg cca gct gcg	3398			
215	Gln Glu Gly Pro Gly Ser Gly Ser Pro Arg Gly Lys Ala Pro Ala Ala				
216	975 980 985				
217	gtg gca gag aag agc cct gtg cga gtg cgg ccc ccg cgt gtc ctg gac	3446			
218	Val Ala Glu Lys Ser Pro Val Arg Val Arg Pro Pro Arg Val Leu Asp				
219	990 995 1000				
220	ggc ccc ggg cct gct ggg atg gcc gcc aca tgc atg aag tgt gtg gtg	3494			
221	Gly Pro Gly Pro Ala Gly Met Ala Ala Thr Cys Met Lys Cys Val Val				
222	1005 1010 1015 1020				
223	gga tcc tgc gcc ggc gtg aac acc ggg ggc ctg cag agg gag cgg cca	3542			
224	Gly Ser Cys Ala Gly Val Asn Thr Gly Gly Leu Gln Arg Glu Arg Pro				
225	1025 1030 1035				
226	ccc agc ccg ggg cct gca agc agg cag gca gcc att cgc cag cag ccc	3590			
227	Pro Ser Pro Gly Pro Ala Ser Arg Gln Ala Ala Ile Arg Gln Gln Pro				
228	1040 1045 1050				
229	cgg gcc cgg gct gac tca ctg ggg gcc ccc tgc tgt ggc ctg gac cct	3638			
230	Arg Ala Arg Ala Asp Ser Leu Gly Ala Pro Cys Cys Gly Leu Asp Pro				
231	1055 1060 1065				
232	cac gct atc ccg ggg aga agc aga gag gcc ccc aag ggt cct ggg gcc	3686			
233	His Ala Ile Pro Gly Arg Ser Arg Glu Ala Pro Lys Gly Pro Gly Ala				
234	1070 1075 1080				
235	tgg agg cag ggt cca ggc ggt agc ggc tcc atg tcc tcg gac tcc agc	3734			
236	Trp Arg Gln Gly Pro Gly Gly Ser Gly Ser Met Ser Ser Asp Ser Ser				
237	1085 1090 1095 1100				
238	agc cca gac agc ccg ggc atc ccc gaa agg tcc ccc cgc tgg cct gag	3782			
239	Ser Pro Asp Ser Pro Gly Ile Pro Glu Arg Ser Pro Arg Trp Pro Glu				
240	1105 1110 1115				

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 2,41,42

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10784089.raw.txt

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L:798 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:801 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:32